

**STIC Biotechnology Systems Branch****RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,102A  
 Source: IPWO  
 Date Processed by STIC: 07/07/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

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# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/560, 102 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

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## RAW SEQUENCE LISTING

DATE: 07/07/2006

PATENT APPLICATION: US/10/560,102A

TIME: 16:59:18

Input Set : A:\10560102-Seq List.txt

Output Set: N:\CRF4\07072006\J560102A.raw

Does Not Comply  
Corrected Diskette Needed

Cpg-1)

Gf22137 Response is  
Artificial or Unknown  
Pls Explain the Source  
of genetic Material.  
See Item 10 on  
Error Summary  
Sheet.

4 <110> APPLICANT: Yuki YAMADA  
5 Masashi OGASAWARA  
6 Kaoru HIROKI  
7 Chiaki SAITO  
9 <120> TITLE OF INVENTION: Seasoning  
11 <130> FILE REFERENCE: 506.45680X00  
13 <140> CURRENT APPLICATION NUMBER: 10/560,102A  
14 <141> CURRENT FILING DATE: 2005-12-09  
16 <150> PRIOR APPLICATION NUMBER: JP2003-164747  
17 <151> PRIOR FILING DATE: 2003-06-10  
19 <160> NUMBER OF SEQ ID NOS: 1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 9  
23 <212> TYPE: PRT  
24 <213> ORGANISM: Artificial sequence  
26 <220> FEATURE:  
27 <221> NAME/KEY: UNSURE  
28 <222> LOCATION: (3)...(3)  
29 <223> OTHER INFORMATION: Xaa stands for any amino acid  
31 <220> FEATURE:  
32 <221> NAME/KEY: UNSURE  
33 <222> LOCATION: (5)...(6)  
34 <223> OTHER INFORMATION: Xaa stands for any amino acid  
36 <220> FEATURE:  
37 <221> NAME/KEY: UNSURE  
38 <222> LOCATION: (8)...(9)  
39 <223> OTHER INFORMATION: Xaa stands for any amino acid  
41 <400> SEQUENCE: 1  
W--> 42 Gly Pro Xaa Gly Xaa Xaa Gly Xaa Xaa  
43 1 5

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/560,102A

DATE: 07/07/2006  
TIME: 16:59:19

Input Set : A:\10560102-Seq List.txt  
Output Set: N:\CRF4\07072006\J560102A.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3,5,6,8,9

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**VERIFICATION SUMMARY**

**PATENT APPLICATION:** US/10/560,102A

**DATE:** 07/07/2006

**TIME:** 16:59:19

**Input Set :** A:\10560102-Seq List.txt

**Output Set:** N:\CRF4\07072006\J560102A.raw

L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

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